

OM of: US-09-652-292-2 to: N_Geneseq_1101.* out_format : pfs
Date: Mar 15, 2002 7:56 AM
About: Results were produced by the GenCore software, version
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Command line parameters:
-MODEL=frame+P2n.model
-O=/cgn2_1/USPTO_spool/US09652292/runat_13032002_161726_3249/app_query.fasta_1.606
-DB=N_Genesec_1101 -GFMT=fastap -SUFFIX=tn9 -GAPOPT=12_000
-CAPEXT=4.000 -MINWATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blomsum62
-TRANS=human40.cdi -LIST=45 -DocalIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM_ext -HEARSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09652292 -CGN1_1_238 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLXPY -WAIT -THREADS=1

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Search Information block:

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Search information block:
Query: US-09-652-292-2
Query length: 541
Database: N_Geneseq_1101:*
Database sequences: 930621
Database length: 428662619
Search time (sec): 111.030000
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score_list:

[illegible]

/SIDS2/gcgdata/geneseq/NA2000.DAT.AAC65871 +	375.50	438.58	2.4e-16	2856
/SIDS2/gcgdata/geneseq/NA2000.DAT.AAC45298 +	373.50	441.02	1.7e-16	1685
/SIDS2/gcgdata/geneseq/NA2000.DAT.AAC45290 +	373.50	440.71	1.8e-16	1743
/SIDS2/gcgdata/geneseq/NA1991.DAT.AAQ11148 +	371.50	434.67	3.9e-16	2587
/SIDS2/gcgdata/geneseq/NA2001.DAT.AAH53274 +	356.00	424.84	1.4e-15	987

seq_name: /SIPDS2/acadata/qenegeq/qenegeq/NA1999.DAT: AAX35516

seq_documentation_block:
ID AAX35516 standard: CDNA: 2471 BP.

AC .AAX35516:

DT 08-JUL-1999 (first entry)

xx cDNA encoding facilitative glucose transporter protein GLUT8.

Facilitative glucose transporter protein: GLUT8: malignancy: XX KW

KW breast cancer; prostate cancer; epithelial cell cancer;
KW non-insulin-dependent diabetes mellitus; insulin resistance;

KW central obesity; hypertension; dyslipidaemia; glucose intolerance
KW cancer: es

XX Homo sapiens

XX
PN
W09918125-A1XX
15-APR-1999XX
DE 30-SEP-1998.XX
PP 01-OCT-1997. 97AII-0009573XX
PA (SVIN -) ST VINCENTS INST MEDXX
PT Best JD. Rogers SD:

XX
DR
wpt: 1999-277253/23

DR P-PSDH; AAY02108.
XX

Pt **Nucleic Acid encoding**

PS
Claim 4; Page 61-62; 1/2pp; English: xx

CC The present sequence encodes a facilitative glucose transporter
CC protein. GLUT8 Agents that inhibit activity or expression of

CC sequences or dominant negative mutants) are used to treat CC (particularly non-utilizable glucose analogues, antilipase

CC malignancy, particularly cancer of breast, prostate and epithelial cells (e.g. skin or colon). Agents that upregulate expression of

CC (e.g. the GLUT8 gene, administered by tissue-localized gene therapy) used to treat non-insulin-dependent diabetes mellitus and/or for

CC resistance (e.g. central obesity, hypertension, dyslipidaemia or CC intolerance). Detecting expression of GLUT8 is used for diagnosing

CC monitoring and staging of cancers, particularly of the breast. CC raised against CLU8 are useful as immunoscreening reagents and as

CC
therapeutic inhibitors,
xx

5Q Sequence 24/1 BP; 611 A; 613 C; 526 G; 678 T; 43 Other;

alignment_scores:			
	Quality:	Length:	
	Ratio:	Gaps:	
	Percent Similarity:	Percent Identity:	

alignment_block:

US-09-652-292-2 x AAX35516

Align seg 1/1 to: AAX35516 from: 1 to: 2471

6 ProValLeuProLeuCysAlaSerValSerLeuLeuGly...GlyLeuTh 21

```

229 CCAGCATTTAGGATTTCTTCTCTATATCTTGTGGTGTGCTCTTGC 278
21 r.....PheGlyTyrGluLeuAlaValIleS 30
279 AGGCCCATCTACGGGATAGGTGGTCTCAGTG...GTGGGCA 325
30 erGly.....AlaLeuLeuProLeuGlnLeuAsp 39
326 CCGGCTTTGTTCTTGCCTCTCTCGAGCTCTCTTGGCGCTCGCTG 375
40 PheGlyLeuSerCysLeuGluGlnGluPhe.....LeuValGI 52
376 TTCACATCAATCCCTTGAACGCTGACCTGTGGCTGGCATTTGGCGC 425
52 yserLeuLeuGly...AlaLeuLeuAlaSerLeuValGlyGlyPheL 68
426 AGTCTGTGCTGGCCATCCTCTCTGCTGCTGCTGCTGCTGCTGCTG 471
68 eulleaspCysTyrGlyArgGlyGlnAlaIleLeuGlySerAsnLeuVal 84
472 .....AGCACGCCAGAGCGGAGATCAGCTGGTC 501
85 LeuLeuAlaGlySerLeuThrLeuGlyLeuAlaGlySerLeuAlaTrpLe 101
502 CACGGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 542
101 u.....ValLeuGlyArgAlaValV 108
543 CCAGGTATGCCCTTGAGGGACTGAGGTGACATCTCTGGG. 582
108 alGlyPheAlaIleSerLeuSerSerMetAlaCysCysIleTyrValSer 124
582 ..... 582
125 GluLeuValGlyProArgGlnArgGlyValLeuValSerLeuTyrGluAl 141
583 .....ATGGGAGCTCGACAGGTGGAGAGAGAGCGCGCACTCCGGCC 626
141 aGlyIleThrValGlyIleLeuLeuSerTyrAlaLeuAsnTyrAlaLeuA 158
627 GGGATTCGGGCTCAGCATCTCTCTGCTATATTTTCAAAATAGGCATTG 676
158 laGlyThrProTrpGlyTyrArgHisMetPheGlyTyrAlaThrAlaPro 174
677 CCAATGTTTCCATGCTGGAAGTACATGTTGGTCTTGTGATTCCTCTG 726
175 AlaValLeuGlnSerLeuSerLeuPheLeuProAlaGlyThrAspGI 191
727 GGAGTTTTCAGCAATTCGAATGATTTTCTTCTCTCCCAAGC..... 768
191 uThrAlaThrHisLysAspLeuIleProLeuGlnGly.....GlyGluA 206
769 .....CCTCGGTTTCTGCTGATGAAGGACAGAGAGAGGAGCTG 805
206 laProLysLeuGlyProGlyArgProArg..... 215
806 CTAGCAAGGTT...CTTGAAGGTAAAGAGACACTCTCAGATACAACTGAG 852
216 .....TyrSerPh 218
853 GAACCTACCTGTGATCAAAATCCTCCCTGAAGATGAATATCACTACAGTTT 902
218 eLeuAspLeuPheArgAlaArgAspAsnMetArgGlyArgThrValG 235
903 TTGGGATCTGTTTCGTTCAAAAGACAACATGCGGACCCCAATAATGATAG 952
235 lyLeuGlyLeuValLeuPheGlnLeuThrGlyGlnProAsnValLeu 251
953 GACTAACACTAGTATTTTGTACAAATCACTTGGCCCAACCAACATATTG 1002
252 CysTyrAlaSerThrIlePheSerSerValGlyPheHisGlyGlySerS 268
1003 TTCATGATCACTCACTGTTTGAAGTCAGTTGGATTTCAAGCAATGAGGC 1052

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268 rAlaValLeuAlaSerValGlyLeuGlyAlaValLysValAlaAlaThrL 285
1053 AGCTAGCTCGCTCCCTCCACTGGGTTGGAGTCGTCAGGTCAATTAGCACCA 1102
285 eutHrAlaMetGlyLeuValAspArgAlaGlyArgAlaLeuLeuLeu 301
1103 TACTGTGCCACTCTTCTTGTAGACCATGTGGCAGCAAAACATTCCTCTGC 1152
302 AlacGlyCysAlaLeuMetAlaLeuSerValSerGlyIleGlyLeuValS 318
1153 ATTGGC.....TTGCTAAATGCTGGATTAAAGCCACACTGA 1187
318 rPheAlaValProMetAspSerGlyProSerCysLeuAlaValProAsnA 335
1188 ATACCAAGATAGTCACAGAC..... 1206
335 laThrGlyGlnThrGlyLeuProGlyAspSerGlyLeuLeuGlnAspSer 351
1207 .....CCTGGGGAC..... 1215
352 SerLeuProProIleProArgThrAsnGluAspGlnArgGluProIleLe 368
1216 .....GTCCCA..... 1221
368 uSerThrAlaLysLysThrLysProHisProArgSerGlyAspProSera 385
1221 ..... 1221
385 laProProArgLeuAlaLeuSerSerAlaLeuProGlyProProLeuPro 401
1221 ..... 1221
402 AlaArgGlyHisAlaLeuLeuArgTyrThrAlaLeuLeuCysLeuMetVa 418
1222 .....GCTTTTGTAAATGGCTGCTCTTAGCCAGCTGTCTTGT 1259
418 lPheValSerAlaPheSerPheGlyPheGlyProValThrTyrLeuValL 435
1260 TTATGTTGCTGCTTTTCAATGGTCTAGACCAATGCCCTGGCTGGTGC 1309
435 euSerGluIleTyrProValGluIleArgGlyArgAlaPheAlaPheCys 451
1310 TCAGCGAGATCTTCTCTGCTGGATCAGAGGACGAGCCATGGCTTTAACT 1359
452 AsnSerPheAsnTrpAlaAlaAsnLeuPheIleSerLeuSerPheLeuAs 468
1360 TCTAGCATCACTGGGGCATCAATCTCCTCATCTCGCTGCACATTTTG.. 1407
468 pLeuIleGlyThrIleGlyLeuSerTyrThrPheLeuLeuTyrGlyLeu 485
1408 .ACTGTAATCTTATGGCTGCCATGGGTGCTTTTATATATACANTCA 1456
485 hrAlaValLeuGlyLeuGlyPheIleTyrLeuPheValProGluThrLys 501
1457 TGAGTCTAGCATCCCTGCTTTTGTGTTGTTATGTTTATACCTGAGACAAAG 1506
502 GlyGlnSerLeuAlaGluIleAspGlnGlnPheGlnLys 514
1507 GGATGCTCTTTTGGAAACAATATCAATGGAGCTAGCAAAA 1545

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seq_name: /SIDS2/gcgdata/geneseq/geneseq/NA2001.DAT:AAF5868

seq_documentation_block:

ID: AAF5868 standard; cDNA; 2177 BP.

XX AAF5868;

AC

XX

DT 17-APR-2001 (first entry)

XX Human GLUTX2 coding sequence.

DE Human; GLUTX; gene therapy; vaccine; hexose transport modulator;

XX KW


```

353 LeuProProIleProArg.....ThrAsnGluAsp..... 362
1629 TGTGTTCCAGTTAATAAGCATCTACAAATGAGCGACCTGGGCGAGGTG 1678
363 GlnArgGluProIleLeuSerThr.....AlaLysLysT 374
1679 TGAAGTGAACCAAGTTTCAACAAAGAGATATATTTTGGGCTTCAAT 1728
374 hrLysProHisProArgSerGlyAspProSerAlaProProArgLeuAla 390
1729 TCTGCCCTACTCCATCTCC..... 1748
391 LeuSerSerAlaLeuProGlyProProLeuProAlaArgGlyHisAlaLe 407
1748 ..... 1748
407 uLeuArgTrpThrAlaLeuLeuCysLeuMetValPheValSerAlaPheS 424
1749 .....TGGACTGCTCTTGGGCTTATTTTATATCTTCTCTCTTTG 1791
424 erPheGlyPheGlyProValTrpLeuValLeuSerGluIleTyrPro 440
1792 CACCTGGAATGGGACCACTGGACTGTAATTTCTGAATATATATATCCC 1841
441 ValGluIleArgGlyArgAlaPheAlaPheCysAsnSerPheAsnTrpAl 457
1842 CTTTGGGCAAGAGTACAGGAATGCAATGTCATCTGGAATAAACTGGAT 1891
457 aAlaAsnLeuPheIleSerLeuSerPheLeuAspLeuIleGlyThrIleG 474
1892 TTTCAATGCTCTGCTTTCATCAATATTTTACACAGCAGATATCTTA 1941
474 lyLeuSerTrpThrPheLeuLeuTyrGlyLeuThrAlaValLeuGlyLeu 490
1942 CATACTATGGAGCTTCTCTCTATCTGATTCGATTCGCTGGGACTC 1991
491 GlyPheIleTyrLeuPheValProGluThrLysGlyClnSerLeuAlaG 507
1992 CTTTTCATCTATGCTCTCTCTCTGAGACCAAGGCAAAATAGAGGA 2041
507 uIleAspGlnGlnPheGlnLysArgPheThrLeuSerPheGlyHisA 524
2042 AATTGAATCACTCTTTGACACAGGCTATGATCATGTGGCACTTCAGAT 2091
524 rgGlnAsnSerThrGlyIleProTyrSerArgIleGlu 536
2092 CTGATGAAGGGAGATATATTGAATATATATCCGCGTGAAG 2129

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seq_name: /SDS2/gcgdata/geneseq/geneseq/NA2001.DAT:AAF55869

seq_documentation_block:

ID AAF55869 standard; cDNA: 2504 BP.

AC AAF55869;

XX

DT 17-APR-2001 (first entry)

XX

DE Rat GLUTX2 coding sequence.

XX

KW Rat; GLUTX; gene therapy; vaccine; hexose transporter modulator;
 KW hexose transport disorder; ischaemia; diabetes; hyperglycaemia; ss;
 KW hypoglycaemia; glucose metabolism disorder; neurodegenerative disease.

OS Rattus sp.

XX

PN WO200104145-A2.

XX

PD 18-JAN-2001.

XX

PF 14-JUL-2000; 2000WO-IB01042.

XX

PR 14-JUL-1999; 99US-0143907.

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PR 27-AUG-1999; 99US-0151140.
PR 23-SEP-2000; 2000US-0184285.
PR 13-JUL-2000; 2000US-0616132.
XX
PA (UYLA-) UNIV LAUSANNE.
XX
PI Thorens B, Ibberson M, Uldry M;
XX
DR WPI; 2001-112615/12.
DR P-PSDB; AAB66936.
XX
PT Nucleic acids encoding GLUTX glucose transporter proteins, useful in
PT the prevention, diagnosis and treatment of hexose transport disorders,
PT e.g. ischemia and diabetes.
XX
PS Claim 3; Page 77-79; 124pp; English.
XX
CC The present invention relates to GLUTX proteins (AAF55865-AAF55871 and
CC AAB66932-AAB66941). The GLUTX proteins are related to the facultative
CC glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport
CC function. The GLUTX proteins may be used in the diagnosis, prevention and
CC treatment of hexose transport disorders such as ischaemia, diabetes,
CC hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a
CC neurodegenerative disease. The present sequence is the coding sequence
CC for rat GLUTX2.
XX
SQ Sequence 2504 BP; 547 A; 713 C; 693 G; 551 T; 0 other;

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alignment_scores:

Quality: 547.00 Length: 585
 Ratio: 1.609 Gaps: 15
 Percent Similarity: 58.120 Percent Identity: 30.256

alignment_block:

US-09-652-292-2 x AAF55869

Align seg 1/1 to: AAF55869 from: 1 to: 2504

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4 SerProValLeuProLeuCysAlaSerValSerLeuLeuGlyGlyLe 20
283 ACCCCGCCCTTCGTGTACGCGCGCGGCTCTCTCGGCTCTCGCGGCTT 332
20 uThrPheGlyTyrGluLeuAlaValIleSerGlyAlaLeuLeuProLeuG 37
333 CCGTTCGCTACGACCGCGGTGTGTGCGGGGCGCATGCTCTGCTGC 382
37 InLeuAspPheGlyLeuSerCysLeuGluGlnGluPheLeuValGlySer 53
383 GCGCCAGATGCGCTGGCGCGCATGTGGCAGGAGCTGTGTGTGCGGC 432
54 LeuLeuLeuGlyAlaLeuLeuAlaSerLeuValGlyGlyPheLeuIleAs 70
433 GCGGTGGCGCGCGCGCTGCGCGCGCTGCGCGGAGGCGGCGCTGAACG 482
70 pCystyrGlyArgLysGlnAlaIleLeuGlySerAsnLeuValLeuA 87
483 CGCCCTCGGTGCGGGAAGCGCATCTGTGTGGCAGCGCCCTGTGCACG 532
87 laGlySerLeuThrLeuGlyLeuAlaGlySerLeuAlaTrpLeuValLeu 103
533 TGGGCTCCGCGCTGTGTGGCGCGCGCGCAACAAGGAGACGCTGTGGGC 582
104 GlyArgAlaValValClyPheAlaIleSerLeuSerSerMetAlaCysCy 120
583 GCGCGCGCTGTGTGGGCTCGGCATCGGCATCGCATCATCATGACAGTGC 632
120 sileTyrValSerGluLeuValGlyProArgGlnArgGlyValLeuValS 137
633 CGGTATACATCGCGAGGTCTCTCCACCAACCTGAGAGGTCTGCTGTC 682
137 erLeuTyrGluAlaGlyIleThrValGlyIleLeuLeuSerTyrAlaLeu 153

```

```

683 CCATCAACACCCTCTTCATCACCGGGGACAGCTCTTTGGAGCGTTGTT 732
154 AsnTyrAlaLeuAlaGlyThrProTrrp...GlyTrrpArgHisMetPheG1 169
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
733 GATGGAGCCCTTTAGTTACCTGCAGAGGATGGATGGAGGTACATGTTGG 782
169 yTrrpAlaThrAlaProAlaValLeuGlnSerLeuSerLeuLeuPheLeuP 186
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
783 ACTTGGCGCATTCACCGCGTTATACAAATTCCTCGGATTCCTCTTTTTC 832
186 roAlaGly..... 188
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
833 CCGAAGTCTCTCGGTGGCTGATACAGAAAGGACAGACTCAGAGGCGCCG 882
189 ..... 193
883 CGAATTTTGCACAGATCGGTGGGAATCAGACCATTCAGCAGGAGTATGA 932
193 aThrHisLysAspLeuLeuProLeuGlnGlyGlyGluAlaProLysLeuG 210
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
933 CAGCATCAGGAACAGCATCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 982
210 lYProGlyArgProArgTyrSerPheLeuAspLeuPheArgAlaArgAsp 226
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
983 GACCT.....ATATCTGCAGAAATGCTGAGTTACCCC 1014
227 AsnMetArgGlyArgThrValGlyLeuGlyLeuValLeuPheGlnG1 243
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1015 CCAACTCGCGGCGGATGCTAGCTGGGATGGCTTACAGATGTTCCAGCA 1064
243 nLeuThrGlyGlnProAsnValLeuGlyGlyGlnAlaThrLeuAlaMetGlyLeuValAs 260
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1065 GCTCTCGGCGCATCAACACTATCATGACTACAGCGGACCATCTGCAGA 1114
260 erValGlyPheHisGlyGlySerSerAlaVal...LeuAlaSerValGly 275
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1115 TGTCGCGCGTGGAGATGATAGACTTGCAATATGGCTGGCTTCATT... 1161
276 LeuGlyAlaValLysValAlaAlaThrLeuThrAlaMetGlyLeuValAs 292
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1162 ACAGCCTTACCAATTTTACACTGCTGGTGGCTGGCTGGCTGGCTGG 1211
292 pArgAlaGlyArgArgAlaLeuLeu.....LeuAlaGlyCysAlaL 306
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1212 GAAGGTGGCGCGGAGGAGTACCTTTGGCAGTTTGGCAGGT...ACCA 1258
306 euMetAlaLeuSerValSerGlyLeuLeu..... 316
1259 CAGTAGCACTTACAATTTCTGGCTGGGATTTCTGCTCAGCTCAGGTC 1308
317 .....ValSerPheAlaValProMetAspSerGlyProSerCysLe 330
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1309 TCACACGGGTCACTTTACAGACCAACGGCTCCCTCGGGTCAAAATGCCAC 1358
330 u.AlalValProAsnAlaThrGly.....GlnThrGly 340
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1359 CTCACAGATACAGTACTGTAATGAGTGTATGCTGGATCCAGACTGCG 1408
341 LeuProGlyAspSerGlyLeuLeuGlnAspSerSerLeuProProIlePr 357
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1409 GTTCTGCTACAAGATCAACAGTGTGGCTGCTCAATGATTCCTCTGTGTT 1458
357 oArgThrAsnGlu.....AspGlnArgGluProIleLeuSerThrAlaL 372
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1459 CCGTGAACAAAGCTTCCACCAATGAAGCAGCT.....GGGCGAGGTG 1502
372 yLysThrLysProHisProArgSerGlyAspProSerAlaProProAla 388
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1503 TGAACACGAA.....CCAAAGTTCAAGCAGAGAAG 1531
389 LeuAlaLeuSer.....SerAlaLeuProGlyProProLeuProAl 402
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1532 ATGTTCACTGGGCTTACAGTTTCTGCCCTACCCCA..... 1566

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402 aArgGlyHisAlaLeuLeuArgTrrpThrAlaLeuLeuLeuCysLeuMetValP 419
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1567 .....TACTCTGGACAGCACTCGTGGGCTGGTGTAT 1600
419 heValSerAlaPheSerPheGlyPheGlyProValThrTrrpLeuValLeu 435
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1601 ATCTGTGTTTTCACCCGGAATGGGACCAATGCCCTGGACCGTGGAAC 1650
436 SerGluIleTyrProValGluIleArgGlyArgAlaPheAlaPheCysAs 452
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1651 TCTGAATCTATCTCTCTGGGCAAGAGTACAGGAATCGGTGCTCAGC 1700
452 nSerPheAsnTrrpAlaAlaAsnLeuPheIleSerLeuSerPheLeuAspL 469
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1701 TGAATAAACTGGATTTTCAACGCTGGTGTCTCACTGACCTTTTACACA 1750
469 euIleGlyThrIleGlyLeuSerTrrpThrPheLeuLeuTyrGlyLeuThr 485
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1751 CACCGGAGTATCTTACATACATAGGAGCTTCTTCTTACGCGGATTC 1800
486 AlaValLeuGlyLeuGlyPheIleTyrLeuPheValProGluThrLysG1 502
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1801 GCGCTGTGGAGTCTTTTCTGCTATGGCTGCTCTCTCTGAAACCAAGG 1850
502 yGlnSerLeuAlaGluIleAspGlnGlnPheGlnLysArgArgPheThrL 519
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1851 GAAAAAACTAGAGAAATCGAATCGCTCTTCGACCAACCGCTGTGCACCT 1900
519 euSerPheGlyHisArgGlnAsnSerThrGlyIleProTyrSerArgIle 535
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1901 GCGGACCGCGGACTCGGACGAGGCGGAGTACATCGAGTACATCCCGGTG 1950
536 Glu 536
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1951 AAG 1953
seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT: AAC42332
seq_documentation_block:
ID AAC42332 standard; DNA; 1826 BP.
XX
AC AAC42332;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 35149.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.

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PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-01334256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
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PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
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PR 28-SEP-1999; 99US-0156458.
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PR 06-OCT-1999; 99US-0157865.
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PR 22-OCT-1999; 99US-0160980.
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PR 28-OCT-1999; 99US-0161920.
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Quality: 541.00 Length: 559
Ratio: 1.639 Gaps: 13
Percent Similarity: 59.034 Percent Identity: 28.801

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US-09-652-292-2 x AAC42332 ..

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Align seg 1/1 to: AAC42332 from: 1 to: 1826

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147 ACACCTTACATCATCGACTGCTCTCCGCGGA...ATCGAGGCTC 193

20 uThrPheGlyTyrGluLeuAlaValIleSerGlyAlaLeuProLeuG 37
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
194 TCTCTCGGTACGATACCGGATCAATTCGCGAGCTCTTTTCATCA 243

37 InLeuAspPhe.....GlyLeuSerCysLeuGluGlnPheLeu 50
:: ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
244 AAGAAGATTTTGATGAAGTTGTAAGAAACATGGCTTCAGTCAACTATT 293

51 ValGlySerLeuLeuGlyAlaLeuAlaLeuAlaSerLeuValGlyGlyP 67
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
294 GTTAGTAGTGCAGTGCCTGGAGCATCGTCGGAGCAGCAGTCGGAGGTTG 343

67 eLeuIleAspCysTyrGlyArgLysGlnAlaIleLeuGlySerAsnLeuV 84
::||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
344 GATCAATGATAAGTTGGTAGGAGGATGCGAATCTTATCGCGCATGTTTC 393

84 aLeuLeuAlaGlySerLeuThrLeuGlyLeuAlaGlySerLeuAlaTrp 100
::||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
394 TTTTCTTGATCGTGGGATTTGATGGCATTTGCTCCGCGCTCCTTGGGTT 443

101 LeuValLeuGlyArgAlaValValGlyPheAlaIleSerLeuSerSerMe 117
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167 tPheGlyTyrAlaThrAlaProAlaValLeuGlnSerLeuSerLeuLeuP 184

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195 sLysAspLeuIleProLeuGlnGlyGlyGluAlaProLys.....
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841 CAATCATTTGA.....GATAGCTTCTCT 863

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267 SerSerAlaValLeuAlaSerValGlyLeuGlyAlaValLysValAlaAl 283
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1281 .....TCGAGGTGGAAGTGCATGAAGTGTCTCAGGTCCGAATGTGAT 1324

377 sProArgSerGly...AspProSerAlaProProArgLeuAlaLeuSerS 393
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1325 CTCGCCGACGGGGTACAGCCGTACGCCAGGAGCATGTGTTGGTGTGT 1374

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1475 TTACATCGTAGTCTAGCCACAGGATAGGGACATGTCCCGTGGATCGTCA 1524
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 468 pLeuIleGlyThrIleGlyLeuSerTrpThrPheLeuLeuTyrGlyLeu 485
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 485 hrAlaValLeuGlyLeuGlyPheIleTyrLeuPheValProGluThrLys 501
 1675 TCTCCAGCATCGGCTCTTCTTCATTTGGTGTCTCTTCTTCTGAGACCAA 1724
 502 GlyGlnSerLeuAlaGluIleAspGln 510
 1725 GGGCTTCAGTTTGGAGGAGGTGAGAG 1751

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seq_documentation_block:

ID AAH88793 standard; cDNA; 1905 BP.

AC AAH88793;

DT 28-SEP-2001 (first entry)

DE Sugar transporter cDNA sequence #86.

KW Moss; carbohydrate metabolism related protein; CMRP; sugar; cofactor;
 KW fine chemical production; carbohydrate; polysaccharide; ss.

OS Physcomitrella patens.

XX WO200144476-A2.

XX 21-JUN-2001.

XX 14-DEC-2000; 2000WO-EP12697.

XX 16-DEC-1999; 99US-0171101.

XX (BADI) BASF PLANT SCI CMWB.

XX Lerchl J, Renz A, Ehrhardt T, Reindl A, Cirpus P, Bischoff F;
 PI Frank M, Freund A, Duwenig E, Schmidt R, Reski R;

XX WPI: 2001-398155/42.

XX P-PSDB; AA00107.

PT Novel moss nucleic acid molecules encoding a carbohydrate metabolism
 PT related protein useful for modulating production of fine chemicals such
 PT as carbohydrates, cofactors and enzymes from microorganisms and plants

PS Claim 7; Page 110; 133pp; English.

XX This invention relates to nucleic acid molecules AAH88793
 CC isolated from Physcomitrella patens (a moss), which encode carbohydrate
 CC metabolism related proteins (CMRP) represented in AA00022 - AA00110.
 CC Included in the invention is a vector containing the CMRP cDNA, and a
 CC host cell transformed with the vector. The host cell (a microorganism,
 CC Corynebacterium or Brevibacterium, moss or algae or a plant cell) is
 CC useful for producing a fine chemical such as carbohydrates, cofactors
 CC and/or enzymes. The nucleic acid molecules are suitable for modifying a
 CC carbohydrate production system in a host, e.g., microorganisms and
 CC plants. They are also useful to identify those DNA sequences and enzymes
 CC in other species which are useful to modify the biosynthesis of starch,
 CC cell wall polysaccharides and sugars. The nucleic acid molecules may be

CC utilised in the genetic engineering of Corynebacterium glutamicum and the
 CC related Brevibacterium species and Acetobacter xylinum and Chlorella to
 CC make it a better or more efficient producer of one or more fine
 CC chemicals. Mutagenesis of one or more CMRPs may also result in CMRPs
 CC having altered activities which indirectly impact the production of one
 CC or more desired fine chemicals from plants. Primers AAH8705 - AAH8707
 CC are used in the sequencing of the CMRP cDNA sequences of the invention.

XX SQ Sequence 1905 BP; 402 A; 408 C; 538 G; 557 T; 0 other;

alignment_scores:

Quality: 517.50 Length: 527

Ratio: 1.719 Gaps: 8

Percent Similarity: 57.116 Percent Identity: 28.463

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 23 YTyrgluLeuAlaValIleSerGlyAlaLeu.....LeuProLeuGlnL 38
 153 TTACCATCTCGGGTGGTTAATGTCGATGGAGTACATTTCTAAGGATC 202
 38 euAspPheGlyLeuSerCysLeuGluGlnPheLeuValGlySerLeu 54
 203 TAGGTTTGGCCACGATGCTGTAACACAGGATGGGTGGTAAGCTCAACT 252
 55 LeuLeuGlyAlaLeuLeuAlaSerLeuValGlyGlyPheLeuLeuAspCy 71
 253 CTAGCTGTCGCTACTGTGGTTCCTTACTGGAGCGCCCTGTGTCACA 302
 71 sTyrglyArgLysGlnAlaIleLeuGlySerAsnLeuValLeuAlaG 88
 303 CTTAGGTCGCAAGGTACATTCAGATTACGGCGCTCTTTATTGTGG 352
 88 lySerLeuThrLeuGlyLeuAlaGlySerLeuAlaTrpLeuValLeuGly 104
 353 GCACCTCTCTCAGTGCAAAACACACACGATTCGAGGCTATGGTATTGA 402
 105 ArgAlaValValGlyPheAlaIleSerLeuSerSerMetAlaCysCysII 121
 403 AGAATTTGGTGGTGGATTGGAGTTTCATCTGGTGTTCGCTCT 452
 121 eTyrglySerGluLeuValGlyProArgGlnArgGlyValLeuValSerL 138
 453 ATACATTCGGAGGTCTCGCCACACAGATTCGAGGTACCATCGGGACAT 502
 138 euTyrgluAlaGlyIleThrValGlyIleLeuLeuSerTyrglyAlaLeuAsn 154
 503 TGAATCAGCTCTTATTTGCGTGGTATCTGTTAGCTCTGATTGCTGGC 552
 155 TyrglyAlaLeuAlaGlyThrProTrpGlyTrpArgHisMetPheGlyTrpAl 171
 553 CTTCTTTGGGAGTAACCTGTCTGTCGGCGACCATGTTTGCCTTAGC 602
 171 aThrAlaProAlaValLeuGlnSerLeuSerLeuLeuPheLeuPro.... 186
 603 TACAGTCTCGCTGCTTTTGTGGGTTTAGGCATGGCGTACTGTCGGGAGA 652
 187AlaGlyThrAspGluThrAla 193
 653 GTCCACGCTGGCTATACAGATGGTAAGACCGCAGAGCGGAAACCGCA 702
 194 ThrHisLys.....AspLeuIleProLeu 201
 703 GTAAGGAGACTTTGGGGCAAGCAAGGTCGAGAGTTCAATGGCAGATT 752


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ID  AAZ24474 standard; cDNA: 1862 BP.
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XX  AAZ24474;
AC
XX
XX  17-FEB-2000 (first entry)
DT
XX
XX  Spinach glucose translocator cDNA.
DE
XX
XX  Glucose translocator; spinach; plant; herbicide production;
KW  carbon/nitrogen relationship; starch content; sugar form
KW  starch mobilization; plastid; hexose transport; ss.
XX
XX
OS  Spinacia oleracea.
XX
XX  Key Location/Qualifiers
FH  61..1716
FT  CDS /*tag= a
FT  /product= "glucose translocator"
XX
XX  DE19826444-C1.
XX
XX  18-NOV-1999.
XX
XX  13-JUN-1998; 98DE-1026444.
XX
XX  13-JUN-1998; 98DE-1026444.
XX
XX  (FLUE/) FLUEGGE U.
XX  (SERV/) SERVAITES J.
PA
XX
XX  Fluegge U, Weber A, Fischer K, Servaites J;
PI
XX
XX  WPI; 1999-621474/54.
DR  P-PSDB; AAY50799.
XX
XX  DNA encoding a spinach glucose translocator, plasmids, b
and transformed plant cells -
XX
XX  Claim 1; Fig 1; 12pp; German.
XX
XX  This invention describes a novel DNA sequence (I) contain
XX  region of a glucose translocator (I) or a variant encodi
XX  having the biological activity of the glucose translocat
XX  useful for identification of insertion mutants, for homo
XX  recombination or to express a non-translatable RNA, as a
XX  antisense effect for cosuppression or a ribozyme activi
XX  synthesis of one or more endogenous plastid glucose tran
XX  cell. This is very useful for production of herbicides.
XX  be used to alter the carbon/nitrogen relationship in lea
XX  heterotrophic tissue, in particular to increase starch c
XX  also be used to degrade sugar formation during starch mo
XX  sequences are also useful to isolate DNA encoding homolo
XX  corresponding genomic clones, in particular the correspo
XX  region or partial promoter region for tissue specific ge
XX  (I) and its variants also serve as a target sequence and
XX  a prokaryotic or eukaryotic protein sequence, catalyses
XX  transport of metabolites over membranes, to direct the m
XX  the plastid membrane, plastid stroma or thylakoids. The
XX  also be used to code a mature protein with the biological
XX  glucose translocator, which can be directed to another c
XX  or cellular membrane system. They can also be used to id
XX  substance, which inhibits activity of hexose transport o
XX  plastid membrane. This sequence encodes the spinach gluc
XX  described in the method of the invention.
XX
XX  Sequence 1862 BP: 437 A; 349 C; 469 G; 607 T; 0 other;
SQ

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alignment_scores:

Quality: 507.00 Length: 525
 Ratio: 1.742 Gaps: 10
 Percent Similarity: 55.429 Percent Identity: 29.714

alignment_block:

US-09-652-292-2 x AA224474 ..

Align seg 1/1 to: AA224474 from: 1 to: 1862

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20 uThrPheGlyTyrGluLeuAlaValIleSerGlyAlaLeuProLeuG 37
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
426 TTTGTTGGATATACCTTGCTGGAGCATGTGTAATGAGCTCTGTACTACCTAT 475
37 InLeuAspPheGlyLeu.....SerCysLeuGluGlnGluPheLeuVal 51
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476 CTGCGATTTAGCTATGCTGGCAATACCTGTTTACAGGATGGGTTGTG 525
52 GlySerLeuLeuGlyAlaLeuLeuAlaSerLeuValGlyGlyPheLe 68
:: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
526 AGCATATTACTTCTGCGAGCATGTAGGTTTCATTTACTGGCGGATCTTT 575
68 uLeAspCysTyrGlyArgGlyGlnAlaIleLeuGlySerAsnLeuVal 85
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576 GGCTGATAAGTTTGAAGGACAAAGACCTTCCAGTTAGATGCAATTCCTC 625
85 euLeuAlaGlySerLeuThrLeuGlyLeuAlaGlySerLeuAlaTrpLeu 101
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
626 TTGCAATAGGACCTTCTCTGTGCCACAGCACAAATGTACAGATAATG 675
102 ValLeuGlyArgAlaValValGlyPheAlaIleSerLeuSerMetAl 118
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676 ATGATGTGCTGTTACTTTTGGCATTTGCAATTTGCCATATCATCTGCC 725
118 acCysTyleTyrValSerGluLeuValGlyProArgGlnArgGlyVal 135
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DT 17-OCT-2000 (first entry)
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 15657.
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KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
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 AC AAA65400;
 XX 09-NOV-2000 (first entry)
 XX Brevibacterium lactofermentum gltBD gene SEQ ID NO:5.
 DE Brevibacterium lactofermentum; gltBD: sugar transporter; breeding;
 KW corynebacterium; phosphoenolpyruvate-sugar transport system; PTS;
 KW non-PTS; ds.
 XX Brevibacterium lactofermentum.
 OS WO200037497-A1.
 PN 29-JUN-2000.
 PD 16-DEC-1999; 99WO-JP07078.
 PF 18-DEC-1998; 98JP-0360620.
 PR (AJIN) AJINOMOTO CO INC.
 XX Kanno S, Kimura E, Matsui K, Nakamatsu T;
 XX WPI; 2000-442642/38.

DR P-PSDB; AAB12594.
 XX Sugar transporter gene gltBD of Brevibacterium lactofermentum, useful
 PT for production of coryneform bacteria with altered membrane sugar
 PT transport -
 XX Claim 3; Page 17-21; 26pp; Japanese.
 PS The present invention describes a protein which has transmembrane sugar
 XX transport activity. The protein is specifically a non
 CC phosphoenolpyruvate-sugar transport system (PTS) sugar transporter.
 CC It can be used for in breeding corynebacteria with altered transmembrane
 CC sugar transport. The present represents the Brevibacterium lactofermentum
 CC sugar transporter gltBD gene, which is used in the exemplification of
 CC the present invention.
 XX Sequence 1476 BP; 298 A; 394 C; 372 G; 412 T; 0 other;

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AC AAH65168;

DT 26-SEP-2001 (first entry)

XX C glutamicum coding sequence fragment SEQ ID NO: 203.

XX Coryneform bacterium; amino acid synthesis; vitamin; saccharide;

KW organic acid synthesis; ds.

OS Corynebacterium glutamicum.

XX EP1108790-A2.

PN 20-JUN-2001.

XX 18-DEC-2000; 2000EP-0127688.

PF 16-DEC-1999; 99JP-0377484.

PR 07-APR-2000; 2000JP-0159162.

PR 03-AUG-2000; 2000JP-0280988.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;

PI Tateishi N, Senoh A, Ikeda M, Ozaki A;

XX WPI; 2001-376931/40.

DR P-PSDB: AAG89949.

XX Novel polynucleotides derived from Coryneform bacteria, for identifying

XX mutation point of a gene, measuring expression of a gene, analysing

XX expression profile or pattern of a gene and identifying homologous gene

XX Claim 8; SEQ ID NO: 203; 246pp + Sequence Listing; English.

XX The present invention provides a number of nucleotide and protein

XX sequences from the Coryneform bacterium Corynebacterium glutamicum. These

XX are useful for identifying the mutation point of a gene derived from a

XX mutant of coryneform bacterium, measuring expression amount and

XX analysing the expression profile or expression pattern of a gene derived

XX from Coryneform bacterium, and identifying a homologue of a gene derived

XX from coryneform bacterium. Coryneform bacteria are useful for producing

XX amino acids, nucleic acids, vitamins, saccharides and organic acids,

XX particularly L-lysine. the present sequence is a nucleic acid described

XX in the exemplification of the invention.

XX Note: the sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format directly from the

XX European Patent Office.

XX Sequence 1473 BP; 296 A; 388 C; 377 G; 412 T; 0 other;

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594 CCCAGCAATTGCCCTCTCTTTTGGAACTCTCCGAGTTCAGAAATCCCCA 643
189ThrAspGluThr....AlaThrHisLys 196
644 GCTGGCTTTGTGACGAGGACGCATGATGAGGCTCGCGCAATTCCTGAA 693
197 AspleuIleProLeuGlnGlyGlyGluAla..... 206
694 ACCATTGCCCTCTAGACGTGCCCATGCCAGATGCTGTGATGTTGAACA 743
207ProLysLeuGlyProGlyArgProArgTyrSerPheLeuA 220
744 CCTAGCAAGAGAACGACGCGCTTTCGAGAAAGTCCATGGCTTAAGGG 793
220 sPLeuPheArgAlaAraAspAsnMetArgGlyArgThrValGlyLeu 236
794 AAATTTTGTCCAGCAAGTGGCTTGTGGGC...ATCCTCCTGGTAGGTATC 840
237 GlyLeuValLeuPheGlnLeuThrGlyGlnProAsnValLeuCysty 253
841 GGATTGGGTGTCGCACAGCAGCTCACCGGCATCAACTCCATCATGCTACTA 890
253 rAlaSerThrIlePheSerSerValGlyPheHisGlyGlySerSerAlaV 270
891 CGGCCAGGTGTCTCATTTAGGCTGGTTTC...TCCGAGAAATGCAGCT 937

[illegible]

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seq_documentation block:

ID AAH64966 standard; DNA; 349980 BP.

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AC ААН64966;

XX

DT 26-SEP-2001 (first entry)

XX
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DE C glutamicum coding sequence fragment SEQ ID NO: 1.
XX
KW Corynebacterium: amino acid synthesis: vitamin: saccharide:


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387 ProArgLeuAlaLeuSerSerAlaLeuProGlyProLeuProAlaAr 403
191060 ..... 191060
403 gGlyHisAlaLeuLeuArgTrpThrAlaLeuLeuCysLeuMetValPheV 420
191059 ..... 191059
420 aLserAlaPheSerPheGlyPheGlyProValThrTrpLeuValLeuSer 436
191028 TGGGATCCATGCAGACCTTCCTCAACGTAGCTACCTGGGTTATGCTCTCT 190979
437 GluIleTrpProValGluIleArgGlyArgAlaPheAlaPheCysAsnSe 453
190978 GAGCTCTCCCGCTGGCAATGCGGTTTCGCAATCGGTATCTCAGTGT 190929
453 rPheAsnTrpAlaAlaAsnLeuPheIleSerLeuSerPheLeuAspLeuI 470
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470 leGlyThrIleGlyLeuSerTrpThrPheLeuLeuTyrcGlyLeuThrAla 486
190878 TGGAGCAGTAGGACTTAACCGAACCCTTCTTCATGTCGCCGAATCGGT 190829
487 ValLeuGlyLeuGlyPheIleTyrcLeuPheValProGluThrLysGlyG 503
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ID AA32202 standard; cDNA; 1960 BP.
AC AA32202;
DT 14-JAN-2000 (first entry)
DE Soybean hexose carrier protein encoding cDNA.
KW Hexose carrier protein; corn; rice; sorghum; soybean; wheat;
KW carbohydrate transport; plant carbon partitioning; manipulation;
KW carbohydrate distribution; ss.
OS Glycine max.
XX WO9953082-A2.
XX 21-OCT-1999.
XX 07-APR-1999; 99WO-US07561.
XX 09-APR-1998; 98US-0081131.
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX Allen SM, Lightner JE, Rafalski JA, Thorpe CJ;
XX WPI; 1999-620438/53.
XX P-PSDB; AY40632.
XX New hexose carrier proteins used to manipulate carbohydrate transport
PT
PT Claim 2; Page 46-47; 60pp; English.
PS

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XX The present sequence encodes a hexose carrier protein from the
CC invention, which describes hexose carrier proteins isolated from sorghum,
CC rice, wheat, soybean and corn. Also described are: (1) a chimeric gene
CC comprising a hexose carrier protein polynucleotide operably linked to
CC regulatory sequences; (2) a transformed host cell comprising the chimeric
CC gene; and (3) altering the level of expression of a hexose carrier
CC protein in a host cell, comprising transforming a host cell with the
CC chimeric gene and growing the cell under expression conditions. Hexose
CC carrier proteins may be used to manipulate carbohydrate transport and to
CC alter whole plant carbon partitioning or to manipulate carbohydrate
CC distribution between cellular compartments.
XX
SQ Sequence 1960 BP; 481 A; 413 C; 456 G; 601 T; 9 other;

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Ratio: 1.657 Gaps: 14
Percent Similarity: 51.801 Percent Identity: 27.616

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18 yGlyLeuThrPheGlyTyrcGluLeuAlaValIleSerGly.....AlaL 33
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248 TGGGTTAATCTTCGGTTACGATATCGGAATTCAGGTGGGTGCATCCA 297
.. |||... ||| ||| ||| ..|||...

33 euLeuProLeuGlnLeuAspPheGlyLeuSerCysLeuGluGlnGlu... 48
.. |||... ||| ||| ||| ..|||...

298 TGGATCCGTTTCTGCTCAAGTTTTCCTCCGTCGGTGTTCGGAAGAAGAT 347
48 .....

348 TCCGACAAAACGGTGAACCACTACTGTCAATACGACAGTCAGACACTGAC 397

49 .PheLeuValGlySerLeuLeuLeuGlyAlaLeuLeuAlaSerLeuValG 65
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398 GATGTTACGTCGCTGTATCTGCGCCGCTGCTGCTGCTGCTGCTGCTG 447

65 yGlyPheLeuIleAspCysTyrcGlyArgLysGlnAlaIleLeuGlySer 81
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448 CTTCCACCGTCACAGTACGTTGCGCCGGAATTCCTCATGCTTTTCGGA 497

82 AsnLeuValLeuAlaGlySerLeuThrLeuGlyLeuAlaGlySerLeu 98
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498 GGCTTGCTTTCTCGNCGGTCCTTATCAACGGNTTGGCCACACAGT 547

98 uAlaTrpLeuValLeuArgAlaValValGlyPheAlaIleSerLeuS 115
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548 GTGGTTCATCGTGGTGGGTCGATCTGCTCGGTTTCGGTATCCGGTTG 597

115 erSerMetAlaCysCysIleTyrcValSerGluLeuValGlyProArgGln 131
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598 CCAATCAGTCTGTGCCACTCTANCTATCTGAATGGCTCCATACAATAT 547

132 ArgGlyValLeuValSerLeuTyrcGluAlaGlyIleThrValGlyIleLe 148
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648 AGAGGAGCATTCGAACATGGCTTTCAGTTGTCATCCTCCTGTTGATCCT 697

148 uLeuSerTyrcAlaLeuAsnTyrcAlaLeuAlaGlyThrPro.....TrpG 163
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698 TGTGCCAATGTTGTAACATATTTCTTCTTAAATCAAAAGGTGGTGGG 747

163 yTrpArgHisMetPheGlyTrpAlaThrAlaProAlaValLeuGlnSer 179
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748 GATGGAGGTTGAGTTGGGAGGTGCTATGCTCCCTCCCTTATATATCACA 797

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180 LeuSerLeuLeuPheLeuProAlaGlyThrAspGluThrAlaThrHisLy 196
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798 GTAGATCACTAGTCTTCCA.....GACATCCCAA 829
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196 SASPLEuLeuProLeuGlnGlyGluAlaProLysLeuGlyProGlyA 213
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830 TTCCATGATTGAAGGGGTGATCGCAGAGAGGCAAGGCTCAGCTTCAGA 879
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213 rGProArg.....TyrSerPheLeuAspLeuPheArg 223
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880 GAATTCGCGCATCGACAAATGTTGATGAAGAGTTCAATGACCTTGTGGCA 929
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224 AlaArgAspAsn..... 227
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930 GCAAGTAGAATCTCTAGCCAAGTGGAGCACCCCTTGGAGGAACCTTGTGCA 979
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228 .....MetArgGlyArgThrThrValGlyLeuGlyLeuValLeuPheG 242
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980 AACAAGTACAGACCCACCTCACCATGCGCTGTGATTCCATTCTTCC 1029
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242 InGlnLeuThrGlyGlnProAsnValLeuCysTyrAlaSerThrIlePhe 258
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259 SerSerValGlyPheHisGlyGlySerSerAlaValLeuAlaSerValG 275
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1080 AGCTCATCGGTTTAAG...GATGATGCTGCTTAATGTGAGCTGTGAT 1126
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275 yLeuGlyAlaValLysValAlaAlaThrLeuThrAlaMetGlyLeuValA 292
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292 sPArgAlaGlyArgArgAlaLeuLeuAlaGlyCysAlaLeuMetAla 308
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1177 ACAAGTGGGTAGGAGACCCCTTTCTTGAAGTGGAGTGCAAAATGCTC 1226
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309 LeuSerValSerGlyIleGlyLeuValSerPheAlaValProMetAspSe 325
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1227 ATT..... 1229
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325 rGlyProSerCysLeuAlaValProAsnAlaThr.....G 337
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337 yGlnThrGlyLeuProGlyAspSerGlyLeuLeuGlnAspSerSerLeu 353
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1292 ..... 1292
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370 rAlaLysLysThrLysProHisProArgSerGlyAspProSerAlaProp 387
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1292 ..... 1292
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404 GlyHisAlaLeuLeuArgThrThrAlaLeu.....LeuCysLeuMe 417
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417 tValPheValSerAlaPheSerPheGlyPheGlyProValThrTrpLeuV 434
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451 CysAsnSerPheAsnTrpAlaAlaAsnLeuPheIleSerLeuSerPheLe 467
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467 uAspLeuIle.....GlyThrIleGlyLeuSerTrpThrPheLeuLeuT 482
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482 yrGlyLeuThrAlaValLeuGlyLeuGlyPheIleTyrLeuPheValPro 498
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499 GluThrLysGlyGlnSerLeuAlaGluIleAspGlnGlnPheGlnLysAr 515
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AC AAC50883;
XX
DT 18-OCT-2000 (first entry)
XX
KW Arabidopsis thaliana DNA fragment SEQ ID NO: 56487.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway;
XX metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123548.
XX 23-MAR-1999; 99US-0125788.
XX 25-MAR-1999; 99US-0126264.
XX 29-MAR-1999; 99US-0126785.
XX 01-APR-1999; 99US-0127462.
XX 06-APR-1999; 99US-0128234.
XX 08-APR-1999; 99US-0128714.
XX 16-APR-1999; 99US-0129845.
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XX 23-APR-1999; 99US-0130891.
XX 30-APR-1999; 99US-0131449.
XX 30-APR-1999; 99US-0132048.
XX 04-MAY-1999; 99US-0132407.
XX 05-MAY-1999; 99US-0132484.
XX 06-MAY-1999; 99US-0132485.
XX 06-MAY-1999; 99US-0132486.
XX 06-MAY-1999; 99US-0132487.
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XX 14-MAY-1999; 99US-0134221.
XX 14-MAY-1999; 99US-0134370.
XX 18-MAY-1999; 99US-0134768.
XX 19-MAY-1999; 99US-0134941.
XX 20-MAY-1999; 99US-0135124.

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PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
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DT 17-APR-2001 (first entry)

DE Rat GLUTX1 coding sequence.

Rat; GLUTX; gene therapy; vaccine; hexose transport modulator;
KW
hexose transport disorder; ischaemia; diabetes; hyperglycaemia; ss;
KW
hypoglycaemia; glucose metabolism disorder; neurodegenerative disease;
KW

Rattus sp.

PN WO200104145-A2.

PD 18-JAN-2001.

14-JUL-2000;

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PR 23-FEB-2000; 2000US-01

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PI Thorens B, Ibberson M, Uldry M;
XX

DR WPI; 2001-112615/12.

DR P-PSDB; AAB66933.

PT Nucleic acids encoding GLUTX glucose transporter proteins, useful in the prevention, diagnosis and treatment of hexose transport disorders, PT e.g. Ischemia and diabetes -

PS Claim 3; Page 71-73; 124pp; English.

The present invention relates to GLUTX proteins (AAFP5865-AAFP5871 and AAB65932-AAB65941). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention and treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is the coding sequence for rat GLUTX1.

SQ Sequence 2087 BP; 355 A; 673 C; 580 G; 479 T; 0 other;

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DT 17-OCT-2000 (first entry)
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 KW protein identification; signal transduction pathway;
 KW metabolic pathway; promoter; termination sequence; ss.
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858 GGTCAACGCCCTCATGTTCTATGCAGACCATCTTTGAAGAGGCCAAGT 907
263 heHisGlyGlySerSerAlaValLeuAlaSerValGlyLeuGlyAlaVal 279
908 TCAGGACAGCAGC.....CTGGCCTCGGTCTGCTGGGTGTCATC 948
280 LysValAlaAlaThrLeuThrAlaMetGlyLeuValAspArgAlaGlyAr 296
949 CAGGTGCTGTTCACAGCTGGCGGCTCTCATCATGGACAGACAGGGCG 998
296 gArgAlaLeuLeuAlaGlyCysAlaLeuMetAlaLeuSerValSerG 313
999 GAGCTGCTCTGCTGCTGTGAGGTGTGCTCATGTGTTTCAGCAGAGTG 1048
313 lylLeGlyLeuValSerPheAlaValProMetAspSerGlyProSerCys 329
1049 CCTTCGCC..... 1056
330 LeuAlaValProAsnAlaThrGlyGlnThrGlyLeuProGlyAspSerG1 346
1056 1056
346 yLeuLeuGlnAspSerSerLeuProProIleProArgThrAsnGluAspG 363
1056 1056
363 lNArgGluProIleLeuSerThrAlaLysLysThrLysProHisProArg 379
1057GCCTACTTCAAGCTGACCCAG..... 1077
380 SerGlyAspProSerAlaProProArgLeuAlaLeuSerSerAlaLeuPr 396
1078 ...GGTGCCCTGGCAACTCTCGCAGCTGGCCATCTCGGCGCTGTCTC 1124
396 oGlyProProLeuProAlaArgGlyHisAlaLeuLeuArgTrpThrAlaL 413
1125 TGCACAGCTGTGTATGCC.....AGCGTGGGCTGGCCTGGCTGCCG 1168
413 euLeuCysLeuMetValPheValSerAlaPheSerPheGlyPheGlyPro 429
1169 TGGCAGCATCTGCCTCTTCATGCCCGCTTTCGGGTGGCTGGGGGCC 1218
430 ValThrTrpLeuValLeuSerGluIleTyrProValGluIleArgGlyAr 446
1219 ATCCCTGGCTCTCATGTGTCAGATCTCCCTCTGCATGTCAAGGCGT 1268
446 gAlaPheAlaPheCysAsnSerPheAsnTrpAlaAlaAsnLeuPheIleS 463
1269 GCGACAGGCATCTGCGTCTCACCACCTGGCTCATGGCCTTCTCTGTGA 1318
463 erLeuSerPheLeuAspLeuIleGlyThrIleGlyLeuSerTrpThrPhe 479
1319 CCAAGGAGTTCAGACGCTCATGGAGGTCTCAGGCCCTATGGACCTTC 1368
480 LeuLeuTyrGlyLeuThrAlaValLeuGlyLeuGlyPheIleTyrLeuPh 496
1369 TGCCTTGCCTCGCTTCTGCATCTCATGTCTTCTTCTTCTGCTG 1418
496 eValProGluThrLysGlyGlnSerLeuAlaGluIleAspGlnGlnPheG 513
1419 TGTCCCTGAACATAAGGAAGACTCTGGAACAATACACGCCCATTTTG 1468
513 lNlysArg 515
1469 AGGGCGGA 1476